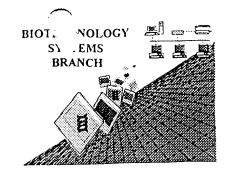# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *09/430,590 C*   *#14*

Source: *1636*

Date Processed by STIC: *3-9-01*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
PATENTIN 3.0 e-mail help: patin3help@uspto.gov **or phone 703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

| **ERROR DETECTED** | **SUGGESTED CORRECTION** | SERIAL NUMBER: 09/430,590C |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ✓ Variable Length
Sequence(s) _1 2_ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism
(NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature
(NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

(handwritten, top left: C. Leffers)

1636

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/430,590C

DATE: 03/09/2001
TIME: 11:58:25

Input Set : A:\ES.txt
Output Set: N:\CRF3\03092001\I430590C.raw

(handwritten stamp:) **Does Not Comply**
Corrected Diskette Needed
See pp. 1,5

```
 3 <110> APPLICANT: Poulter, et al.
 5 <120> TITLE OF INVENTION: UNUSUAL RETROTRANSPOSON FROM THE YEAST CANDIDA ALBICANS
 7 <130> FILE REFERENCE: 674521-2001.1
 9 <140> CURRENT APPLICATION NUMBER: 09/430,590C
10 <141> CURRENT FILING DATE: 1999-10-29
12 <150> PRIOR APPLICATION NUMBER: 60/106,342
13 <151> PRIOR FILING DATE: 1998-10-30
15 <160> NUMBER OF SEQ ID NOS: 156
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 13
21 <212> TYPE: DNA
22 <213> ORGANISM: Candida albicans
24 <220> FEATURE:
25 <221> NAME/KEY: misc_feature
26 <222> LOCATION: (7)..(7)
27 <223> OTHER INFORMATION: nucleotide 'n' represents the 376 nucleotide sequence in between
28       the inverted repeats of the LTR of TCa1 in Candida albican
31 <300> PUBLICATION INFORMATION:
32 <308> DATABASE ACCESSION NO: AF043301
33 <309> DATABASE ENTRY DATE: 1998-07-21
34 <313> RELEVANT RESIDUES: (1)..(13)
36 <400> SEQUENCE: 1
```

(handwritten right margin:) Variable length error. "n" may only represent a single residue. See #6 on the Error Summary Sheet.

```
W--> 37 tgttcgncga aca                                        13
40 <210> SEQ ID NO: 2
41 <211> LENGTH: 19
42 <212> TYPE: DNA
43 <213> ORGANISM: Candida albicans
45 <220> FEATURE:
46 <221> NAME/KEY: misc_feature
47 <222> LOCATION: (10)..(10)
48 <223> OTHER INFORMATION: nucleotide 'n' represents the 382 nucleotide sequence in between
49       the inverted repeats of the LTR of another element in Candida alb
50       ican
53 <300> PUBLICATION INFORMATION:
54 <308> DATABASE ACCESSION NO: Y08494
55 <309> DATABASE ENTRY DATE: 1997-08-27
56 <313> RELEVANT RESIDUES: (1)..(19)
58 <400> SEQUENCE: 2
```

(handwritten right margin:) Variable length error see above.

```
W--> 59 taatgtatan tatacaaca                                  19
62 <210> SEQ ID NO: 3
63 <211> LENGTH: 6426
64 <212> TYPE: DNA
65 <213> ORGANISM: Candida albicans
67 <220> FEATURE:
68 <221> NAME/KEY: CDS
69 <222> LOCATION: (398)..(1372)
```

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MAR 2 2 2001

TECH CENTER 1600/2900

```
70 <223> OTHER INFORMATION: ORF1 coding sequence for gag
73 <220> FEATURE:
74 <221> NAME/KEY: CDS
75 <222> LOCATION: (1373)..(6103)
76 <223> OTHER INFORMATION: ORF2 - coding sequence for pol
79 <400> SEQUENCE: 3
80 tgttggtttg tgcactattt tgtgtcagaa actgatcaat gaaaatgatg gttattatga      60
82 gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt     120
84 ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gggaggagtt     180
86 tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacaa ctagacgtgt     240
88 acacgctcaa tctcaggtaa agaaagttta tattccatca gattagaagt cgatagtgat     300
90 aatcatttcg tcccaaatta gcgttgtata aattcagtcc tcagatttgt attattgatt     360
92 gatagtttcg aagtttgaag gtacagaatt tcacaag atg agt tcc gca aag aat     415
93                                           Met Ser Ser Ala Lys Asn
94                                           1               5
96 gat gat aac gaa ggg aag gtc atg gaa agt gtt gat caa gct aat gct     463
97 Asp Asp Asn Glu Gly Lys Val Met Glu Ser Val Asp Gln Ala Asn Ala
98           10              15              20
100 att agt aag gtg gat gaa cat atc aag gct aga ttc aat atg ctt ttc     511
101 Ile Ser Lys Val Asp Glu His Ile Lys Ala Arg Phe Asn Met Leu Phe
102         25              30              35
104 ata aaa ttt aat gac tta cct aag ttg gcc gtc ggt aat cag aaa agc     559
105 Ile Lys Phe Asn Asp Leu Pro Lys Leu Ala Val Gly Asn Gln Lys Ser
106     40              45              50
108 gtg gat aaa tgg aat gaa gaa ttt aaa tat ttc cac gtt gct tac ccc     607
109 Val Asp Lys Trp Asn Glu Glu Phe Lys Tyr Phe His Val Ala Tyr Pro
110 55              60              65              70
112 gat gtt ttg gaa ttt ttg ctt gac tat aat cct aaa gat aaa ttc aag     655
113 Asp Val Leu Glu Phe Leu Leu Asp Tyr Asn Pro Lys Asp Lys Phe Lys
114             75              80              85
116 gtt aaa aag gta gaa ggt att tat ttt act ggt tgg tgt tta caa atg     703
117 Val Lys Lys Val Glu Gly Ile Tyr Phe Thr Gly Trp Cys Leu Gln Met
118         90              95              100
120 tgt tta cag tcc att ttt gat agg ttc aga ttg atc atg att tct aag     751
121 Cys Leu Gln Ser Ile Phe Asp Arg Phe Arg Leu Ile Met Ile Ser Lys
122         105             110             115
124 cta cca aag cac ttg caa aag gaa gca aac tta atc aaa gct gct tat     799
125 Leu Pro Lys His Leu Gln Lys Glu Ala Asn Leu Ile Lys Ala Ala Tyr
126     120             125             130
128 gat gct gtt act aaa tct aaa gat tat acc att act agt aag atc ttg     847
129 Asp Ala Val Thr Lys Ser Lys Asp Tyr Thr Ile Thr Ser Lys Ile Leu
130 135             140             145             150
132 ctg aag ttt gta aac gtt gaa cat gag tta gtg gtt tgc tat aac ctt     895
133 Ser Lys Phe Val Asn Val Glu His Glu Leu Val Val Cys Tyr Asn Leu
134             155             160             165
136 cca tat ttg ctg cag gtg gaa gag aaa ctt gag gaa ata ctc tac aac     943
137 Pro Tyr Leu Ser Gln Val Glu Glu Lys Leu Glu Glu Ile Leu Tyr Asn
138         170             175             180
140 act tca aac gtt gtc gat gag tat gtc cgt agt ctt cca aat ctc ata     991
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/430,590C

DATE: 03/09/2001
TIME: 11:58:25

Input Set : A:\ES.txt
Output Set: N:\CRF3\03092001\I430590C.raw

```
141 Thr Ser Asn Val Val Asp Glu Tyr Val Arg Ser Leu Pro Asn Leu Ile
142       185                 190             195
144 ggt caa gtc ttg tac ttc aat cat gtg aag aaa tca gag gct tta agt    1039
145 Gly Gln Val Leu Tyr Phe Asn His Val Lys Lys Ser Glu Ala Leu Ser
146       200                 205             210
148 ttg ttt ttg aat att cat gcc tca tac tac tca aag tgg att caa gct    1087
149 Leu Phe Leu Asn Ile His Ala Ser Tyr Tyr Ser Lys Trp Ile Gln Ala
150 215                 220             225                 230
152 gac aat gat aca tca gta ctc cca agt tgc tct acc ata gct gaa gaa    1135
153 Asp Asn Asp Thr Ser Val Leu Pro Ser Cys Ser Thr Ile Ala Glu Glu
154                 235             240             245
156 atg tgt gat cat cct gat tat gct aga ttg gtt gac att cca agc aac    1183
157 Met Cys Asp His Pro Asp Tyr Ala Arg Leu Val Asp Ile Pro Ser Asn
158             250             255             260
160 aaa tat gaa ctt aat ctt att gtt agt tta cca gca cca gag aaa cca    1231
161 Lys Tyr Glu Leu Asn Leu Ile Val Ser Leu Pro Ala Pro Glu Lys Pro
162             265             270             275
164 aaa gga aaa cca gag gag aac tca ctg gaa caa tct caa aag aag aac    1279
165 Lys Gly Lys Pro Glu Glu Asn Ser Ser Glu Gln Ser Gln Lys Lys Asn
166       280             285             290
168 ctg aaa tca aga aag aga aat aag aaa cat cca aaa tca gat aac gat    1327
169 Ser Lys Ser Arg Lys Arg Asn Lys Lys His Pro Lys Ser Asp Asn Asp
170 295             300             305                 310
172 aaa ggt gaa aaa gaa aaa gaa aaa gaa aaa act tca ctg gaa tga aaa    1375
173 Lys Gly Glu Lys Glu Lys Glu Lys Glu Lys Thr Ser Ser Glu     Lys
174             315             320                 325
176 aca ggt gct gct tct att aat tgt gta atg aat ata cat aat tgc agc    1423
177 Thr Gly Ala Ala Ser Ile Asn Cys Val Met Asn Ile His Asn Cys Ser
178             330             335             340
180 aaa acc acg ttt cca gta gaa aat tct cat tct ctt aat gct tct ttg    1471
181 Lys Thr Thr Phe Pro Val Glu Asn Ser His Ser Leu Asn Ala Ser Leu
182             345             350             355
184 aac gta atg aat ttt aaa ggt tta agg ttt aac aag tat cta gtg tat    1519
185 Asn Val Met Asn Phe Lys Gly Leu Arg Phe Asn Lys Tyr Leu Val Tyr
186             360             365             370
188 gat act ggt gcc aca ata tct gtt gtg aac aat aaa gat ata ttg ctg    1567
189 Asp Thr Gly Ala Thr Ile Ser Val Val Asn Asn Lys Asp Ile Leu Ser
190 375                 380             385
192 aat gtt aag gac gca aca att gaa gtt tct gtt gct gat ggt gct aca    1615
193 Asn Val Lys Asp Ala Thr Ile Glu Val Ser Val Ala Asp Gly Ala Thr
194 390                 395             400                 405
196 tta gaa gca gat tgt att ggt gat cta att atc aga gtc ggt att gtc    1663
197 Leu Glu Ala Asp Cys Ile Gly Asp Leu Ile Ile Arg Val Gly Ile Val
198             410             415             420
200 tcg att acg tta gag aat aca ttg tat tta cca gaa agt tcc ttt aat    1711
201 Ser Ile Thr Leu Glu Asn Thr Leu Tyr Leu Pro Glu Ser Ser Phe Asn
202             425             430             435
204 ctt gtg agt ttg aaa caa att gaa gaa cga gga ttt aat gtt ctt att    1759
205 Leu Val Ser Leu Lys Gln Ile Glu Glu Arg Gly Phe Asn Val Leu Ile
```

```
206         440                 445                 450
208 act aaa gaa tca gtg att gta ttt aac caa aat gtg gct cct act att   1807
209 Thr Lys Glu Ser Val Ile Val Phe Asn Gln Asn Val Ala Pro Thr Ile
210     455                 460                 465
212 att gct tca agg aag aat gct gct gat ctt tat atg ggt cct caa ttc   1855
213 Ile Ala Ser Arg Lys Asn Ala Ala Asp Leu Tyr Met Gly Pro Gln Phe
214 470                 475                 480                 485
216 agt gaa gaa tct tta gaa tgt gat ttt gat tat gat ggt ttg gca gat   1903
217 Ser Glu Glu Ser Leu Glu Cys Asp Phe Asp Tyr Asp Gly Leu Ala Asp
218                 490                 495                 500
220 atg ttg tcc aat gct aac caa gat gac aaa gat aaa tca agt atg aat   1951
221 Met Leu Ser Asn Ala Asn Gln Asp Asp Lys Asp Lys Ser Ser Met Asn
222         505                 510                 515
224 gaa atg tca gaa tat caa gaa cat gat tat agt tct cga gca tta ata   1999
225 Glu Met Ser Glu Tyr Gln Glu His Asp Tyr Ser Ser Arg Ala Leu Ile
226         520                 525                 530
228 aat tct ttg acg gag gtt gat gtt tta gat gtt gaa att tcc cca tat   2047
229 Asn Ser Leu Thr Glu Val Asp Val Leu Asp Val Glu Ile Ser Pro Tyr
230     535                 540                 545
232 gga gtt gaa caa ttg cta cca act gga gat aag aac gat att tat aat   2095
233 Gly Val Glu Gln Leu Leu Pro Thr Gly Asp Lys Asn Asp Ile Tyr Asn
234 550                 555                 560                 565
236 ttc cat ttg atg tca aat cat atg tcc att gag aaa atc ttg ttg tta   2143
237 Phe His Leu Met Ser Asn His Met Ser Ile Glu Lys Ile Leu Leu Leu
238                 570                 575                 580
240 caa aaa tac cag ggt ctc gta ctt cac act tca aaa gag agt ctt caa   2191
241 Gln Lys Tyr Gln Gly Leu Val Leu His Thr Ser Lys Glu Ser Leu Gln
242         585                 590                 595
244 aag att gct gat tgt aag gta tgt cta tta tcg aat gcc aaa cag aga   2239
245 Lys Ile Ala Asp Cys Lys Val Cys Leu Leu Ser Asn Ala Lys Gln Arg
246         600                 605                 610
248 agt cac aat cat cat tca gaa aga aaa gcc tcg aga aga cat gag aga   2287
249 Ser His Asn His His Ser Glu Arg Lys Ala Ser Arg Arg His Glu Arg
250     615                 620                 625
252 ctt cat tgt gat act ctc ggt cca ttt agg tcc gaa aat aac aag tgg   2335
253 Leu His Cys Asp Thr Leu Gly Pro Phe Arg Ser Glu Asn Asn Lys Trp
254 630                 635                 640                 645
256 tat tta acg tct gtt ata gat gaa cat acg ggt tac att gaa gga att   2383
257 Tyr Leu Thr Ser Val Ile Asp Glu His Thr Gly Tyr Ile Glu Gly Ile
258                 650                 655                 660
260 att act aaa gac aga aag gta aag gat ctc tta att caa cga tta aag   2431
261 Ile Thr Lys Asp Arg Lys Val Lys Asp Leu Leu Ile Gln Arg Leu Lys
262         665                 670                 675
264 atc tgg aat aat cgg ttt aac gat aag gtg gca tac ttc aga agt gat   2479
265 Ile Trp Asn Asn Arg Phe Asn Asp Lys Val Ala Tyr Phe Arg Ser Asp
266         680                 685                 690
268 aat gct cct gag ttc cca caa cct tct gat tta gct gag ttc ggt att   2527
269 Asn Ala Pro Glu Phe Pro Gln Pro Ser Asp Leu Ala Glu Phe Gly Ile
270     695                 700                 705
```

RAW SEQUENCE LISTING   DATE: 03/09/2001
PATENT APPLICATION: US/09/430,590C   TIME: 11:58:25

Input Set : A:\ES.txt
Output Set: N:\CRF3\03092001\I430590C.raw

```
272 tgg agg gag act ata gcg gca tat ctg cct gag ctt aat ggt ctc gcc   2575
273 Trp Arg Glu Thr Ile Ala Ala Tyr Ser Pro Glu Leu Asn Gly Leu Ala
274 710             715             720             725
276 gag gtt gtt aat aaa ttg att tta caa cag att tac agg atc gtt gtg   2623
277 Glu Val Val Asn Lys Leu Ile Leu Gln Gln Ile Tyr Arg Ile Val Val
278             730             735             740
280 aca ctt ggt cca caa ata ctc aag ttg att tat tat gtg att caa tat   2671
281 Thr Leu Gly Pro Gln Ile Leu Lys Leu Ile Tyr Tyr Val Ile Gln Tyr
282             745             750             755
284 tct att aca atg atc aac cac act cca cgt cgt tca ctc aag gga caa   2719
285 Ser Ile Thr Met Ile Asn His Thr Pro Arg Arg Ser Leu Lys Gly Gln
286         760             765             770
288 acc cct tat ggt tgc tat tat caa tta agt gag gga aat ttc tac cgg   2767
289 Thr Pro Tyr Gly Cys Tyr Tyr Gln Leu Ser Glu Gly Asn Phe Tyr Arg
290     775             780             785
292 ttt cct ttt gcc atc gat tgt gtc gtt aca ttt agt aat gcc atc gaa   2815
293 Phe Pro Phe Ala Ile Asp Cys Val Val Thr Phe Ser Asn Ala Ile Glu
294 790             795             800             805
296 aag aac cgt tac gga gtt aca tca act aaa gga gct cct tca tcg atc   2863
297 Lys Asn Arg Tyr Gly Val Thr Ser Thr Lys Gly Ala Pro Ser Ser Ile
298             810             815             820
300 atg ggt gct gtg att ggc tac gct agc gat tgt ttt agt tat tac gtg   2911
301 Met Gly Ala Val Ile Gly Tyr Ala Ser Asp Cys Phe Ser Tyr Tyr Val
302             825             830             835
304 ttg cta aaa aat atg cgg tgt gat att atc ctt agc cct aat gtc cgt   2959
305 Leu Leu Lys Asn Met Arg Cys Asp Ile Ile Leu Ser Pro Asn Val Arg
306         840             845             850
308 ata ttg cga agc tat gag gtt att aac tcc tat ctc aaa aac tta tcc   3007
309 Ile Leu Arg Ser Tyr Glu Val Ile Asn Ser Tyr Leu Lys Asn Leu Ser
310     855             860             865
312 act aca cct atg tca cac att gtt cct atg gct gaa ggt atc cag gga   3055
313 Thr Thr Pro Met Ser His Ile Val Pro Met Ala Glu Gly Ile Gln Gly
314 870             875             880             885
316 agg caa ctg ggc gct cag tac gag gta cgc gga aca tat gtg gaa agt   3103
317 Arg Gln Ser Gly Ala Gln Tyr Glu Val Arg Gly Thr Tyr Val Glu Ser
318             890             895             900
320 gaa tat gac aat aca aat gac gtg atg cac atg ccc aaa gag tca tat   3151
321 Glu Tyr Asp Asn Thr Asn Asp Val Met His Met Pro Lys Glu Ser Tyr
322         905             910             915
324 tca gtt cag cca gca tcg ttt act tta act acg ggt aac agt tct aac   3199
325 Ser Val Gln Pro Ala Ser Phe Thr Leu Thr Thr Gly Asn Ser Ser Asn
326             920             925             930
328 gaa tat gtt ata aat gat gat cca gta cag att acc att gag aat ccc   3247
329 Glu Tyr Val Ile Asn Asp Asp Pro Val Gln Ile Thr Ile Glu Asn Pro
330     935             940             945
332 gat gat ttt tct aac cct ctt caa cta act gaa gaa tca cac gat atg   3295
333 Asp Asp Phe Ser Asn Pro Leu Gln Leu Thr Glu Glu Ser His Asp Met
334 950             955             960             965
336 gta tcc gaa gta aaa tcg gat gag aat cct aaa ccc agt ctc cac gag   3343
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/430,590C

DATE: 03/09/2001
TIME: 11:58:26

Input Set : A:\ES.txt
Output Set: N:\CRF3\03092001\I430590C.raw

```
L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:59 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:1152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1926 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:2122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:2246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:2266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:2314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:2316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:2318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:2356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:2496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:3147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:3175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:3181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:3183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:3269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:3271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:3429 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:3493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:3543 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:3625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:3645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:3647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:3759 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:3761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:3763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:3765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:3767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:3769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:3821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:3877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:3993 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/430,590C

DATE: 03/09/2001
TIME: 11:58:26

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\03092001\I430590C.raw**

L:3995 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:5079 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85